

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:07:03 ; Search time 22.69 Seconds
(without alignments)
1830.929 Million cell updates/sec

Title: US-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTGDDSRF.....IPCLTMDQSYLWMSDYVI 314

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 segs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_UNCLASSIFIED:*
13: SP_VIRIDIA:*
14: SP_VIRUS:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1641 | 100.0 | 314 | 10 | 043297 arabidopsis |
| 2 | 1611 | 98.2 | 314 | 10 | 042588 arabidopsis |
| 3 | 1215 | 74.0 | 391 | 10 | 042532 arabidopsis |
| 4 | 1208 | 73.6 | 336 | 10 | 039218 arabidopsis |
| 5 | 877 | 53.4 | 347 | 10 | 093544 arabidopsis |
| 6 | 872 | 53.1 | 289 | 10 | 09MA23 arabidopsis |
| 7 | 869 | 53.0 | 294 | 10 | 039533 arabidopsis |
| 8 | 861 | 52.5 | 289 | 10 | 09SDP2 arabidopsis |
| 9 | 849.5 | 51.8 | 312 | 10 | 042538 arabidopsis |
| 10 | 711 | 43.3 | 323 | 10 | 09ZPR4 arabidopsis |
| 11 | 699 | 42.6 | 368 | 10 | 09SIB0 arabidopsis |
| 12 | 649.5 | 39.6 | 315 | 10 | 09SER6 arabidopsis |
| 13 | 647.5 | 39.5 | 272 | 2 | 09JUR6 arabidopsis |
| 14 | 629.5 | 38.4 | 273 | 2 | 09KNT2 arabidopsis |
| 15 | 610.5 | 37.2 | 402 | 10 | 09SLZ8 arabidopsis |
| 16 | 587.5 | 35.8 | 299 | 10 | 09JLR1 arabidopsis |
| 17 | 472.5 | 28.8 | 270 | 3 | 09US33 arabidopsis |
| 18 | 472.5 | 25.7 | 227 | 2 | 032979 mycobacteri |
| 19 | 422.5 | | | | |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 20 | 415.5 | 25.3 | 245 | 2 | 086162 | 086162 synechococ |
| 21 | 409 | 24.9 | 251 | 2 | 069218 | 069218 azotobacter |
| 22 | 405 | 24.7 | 229 | 2 | P95231 | P95231 mycobacteri |
| 23 | 395 | 24.1 | 229 | 2 | 09KGF5 | 09KGF5 bacillus ha |
| 24 | 392 | 23.9 | 258 | 2 | 09KX16 | 09KX16 pseudomonas |
| 25 | 391 | 23.8 | 243 | 1 | 09HHA4 | 09HHA4 methanocarc |
| 26 | 388.5 | 23.7 | 212 | 2 | 09PPF6 | 09PPF6 campylobact |
| 27 | 378 | 23.0 | 191 | 2 | 09LAR1 | 09LAR1 clostridium |
| 28 | 370 | 22.5 | 265 | 2 | 044541 | 044541 azotobacter |
| 29 | 338.5 | 20.6 | 220 | 2 | 09WZD4 | 09WZD4 thermotoga |
| 30 | 312 | 19.0 | 171 | 1 | 09HPR3 | 09HPR3 halobacteri |
| 31 | 307.5 | 18.7 | 305 | 5 | 09U8X2 | 09U8X2 entamoeba h |
| 32 | 298 | 18.2 | 439 | 10 | 09MRF2 | 09MRF2 arabidopsis |
| 33 | 290 | 17.7 | 300 | 5 | 09U8X0 | 09U8X0 entamoeba d |
| 34 | 287 | 17.5 | 305 | 5 | 09U8X1 | 09U8X1 entamoeba d |
| 35 | 265 | 16.1 | 231 | 2 | 091210 | 091210 pseudomonas |
| 36 | 213 | 13.0 | 162 | 2 | 09F7A9 | 09F7A9 salmonella |
| 37 | 207 | 12.6 | 184 | 2 | 09KTI3 | 09KTI3 vibrio chol |
| 38 | 204 | 12.4 | 197 | 2 | 09S138 | 09S138 escherichia |
| 39 | 193 | 11.8 | 275 | 5 | 09GV13 | 09GV13 leishmania |
| 40 | 184.5 | 11.2 | 419 | 2 | 09RDX7 | 09RDX7 legionella |
| 41 | 177.5 | 10.8 | 143 | 2 | 09KTH9 | 09KTH9 vibrio chol |
| 42 | 175 | 10.7 | 236 | 2 | 09X1K7 | 09X1K7 thermotoga |
| 43 | 175 | 10.7 | 240 | 2 | 09K9H8 | 09K9H8 bacillus ha |
| 44 | 168 | 10.2 | 172 | 2 | 09X4C2 | 09X4C2 escherichia |
| 45 | 162.5 | 9.9 | 239 | 2 | 09EZ10 | 09EZ10 staphylococ |

ALIGNMENTS

RESULT 1
ID 043297 PRELIMINARY; PRT: 314 AA.
AC 043297;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
DE (114116.18).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid:3702;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=95154333; PubMed=7851429;
RA Ruffet M.L., Lebun M., Droux M., Douce R.;
RT "Subcellular distribution of serine acetyltransferase from Pisum
RT sativum and characterization of an Arabidopsis thaliana putative
RT cytosolic isoform".
RL Eur. J. Biochem. 227:500-509(1995).
RN [2]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Ruffet M.L., Lebun M., Droux M., Douce R.;
RT Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SOURCE FROM N.A.
RC STRAIN=COLUMBIA;
RX Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altati H., Bel O., Chin C., Chio J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Soultwick A., Thayer A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
RT I.". J. Biol. Chem. 272:10000-10005(1997).
RN [4]
RP Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SOURCE FROM N.A.

RA Ecker J.R.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 Khan S., Kim C., Alatali H., Bel B., Chin C., Chou J., Choi E.,
 Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Thayer A., Tortumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 Theologos A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 CC -i- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-
 SERINE.
 CC EMBL: Z34888; CAA84371.1; -;
 DR EMBL: L34076; AAA58608.1; -;
 DR EMBL: AC002304; AAF79319.1; -;
 DR Mendel: 6700; Arath:1221;6701.
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexapep: 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase; Acyltransferase.
 KM TRANSFERENCE 314 AA; 34251 MW; 78PAC3DA5CE04B0 CRC64;
 SQ

Query Match 100.0%; Score 1641; DB 10; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2,5e-125;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTODDSSRFCCIKNFRGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRTGNTODDSSRFCCIKNFRGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 QY 61 KOEPLISNYVYASTSHRSLESALAHILSVKLSNLPNTLFEFLISVLESPETIEST 120
 DB 61 KOEPLISNYVYASTSHRSLESALAHILSVKLSNLPNTLFEFLISVLESPETIEST 120
 QY 121 KODLIAVERDPACISVYHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 DB 121 KODLIAVERDPACISVYHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 QY 181 VDIHPGAKIGKILLDHATGVIGETAVGDVNSILHGVTLGSTGQSGDRHPKIGDGLV 240
 DB 181 VDIHPGAKIGKILLDHATGVIGETAVGDVNSILHGVTLGSTGQSGDRHPKIGDGLV 240
 QY 241 IGAGSCIIIGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 DB 241 IGAGSCIIIGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 QY 301 DOTSYLEMSDYVI 314
 DB 301 DOTSYLEMSDYVI 314

RESULT 2
 Q42588 PRELIMINARY; PRT; 314 AA.
 ID Q42588;
 AC Q42588;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Murillo M., Foglia R., Diller A., Leustek T.;
 RL Cell Mol. Biol. Res. 0:0-0(0).
 CC -i- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-
 SERINE.
 CC EMBL: L42212; AAC37474.1; -;
 DR Mendel: 6700; Arath:1221;6700.
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexapep: 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase; Acyltransferase.
 KM TRANSFERENCE 314 AA; 34259 MW; A096DF6D2768E21C CRC64;
 SQ

Query Match 98.2%; Score 1611; DB 10; Length 314;
 Best Local Similarity 98.1%; Pred. No. 6.9e-123;
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTODDSSRFCCIKNFRGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRTGNTODDSSRFCCIKNFRGFSVNRKIHHTOIEDDDVWIKMLEAKSDV 60
 QY 61 KOEPLISNYVYASTSHRSLESALAHILSVKLSNLPNTLFEFLISVLESPETIEST 120
 DB 61 KOEPLISNYVYASTSHRSLESALAHILSVKLSNLPNTLFEFLISVLESPETIEST 120
 QY 121 KODLIAVERDPACISVYHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 DB 121 KODLIAVERDPACISVYHCFGLKGFACQAHRIAHITLMKONRKIVALLIONRVSESPA 180
 QY 181 VDIHPGAKIGKILLDHATGVIGETAVGDVNSILHGVTLGSTGQSGDRHPKIGDGLV 240
 DB 181 VDIHPGAKIGKILLDHATGVIGETAVGDVNSILHGVTLGSTGQSGDRHPKIGDGLV 240
 QY 241 IGAGSCIIIGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 DB 241 IGAGSCIIIGNTTIGGAKIGSGSVVVDVPAKRTAVGNPARKLGKKNPKHDKIPCLTM 300
 QY 301 DOTSYLEMSDYVI 314
 DB 301 DOTSYLEMSDYVI 314

RESULT 3
 Q42532 PRELIMINARY; PRT; 391 AA.
 ID Q42532;
 AC Q42532; Q43740; Q43739; 01, Created
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1996 (Tremblrel. 01, Last annotation update)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
 DE (SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SARI PRECURSOR).
 GN SAT-1 OR SAT A.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA MEDLINE=96270381; PubMed=8639741;
 RA Roberts M.A., Wray J.L.;
 RT "Cloning and characterization of an Arabidopsis thaliana cDNA clone encoding an organellar isoform of serine acetyltransferase.";

DR EMBL: D88530; BAA13635.1; -
 DR EMBL: D88529; BAA13634.1; -
 DR Mendel; 10792; Sp101.1221; 10792.
 DR InterPro: IPR001451.
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 347 AA; 37256 MW; FBAB365488DB6B0E CRC64;

Query Match 53.4%; Score 877; DB 10; Length 347;
 Best Local Similarity 56.6%; Pred. No. 2.9e-63;
 Matches 163; Conservative 53; Mismatches 70; Indels 2; Gaps 1;

QY 29 PG--FSVNRKIHHTQIEDDDVWIKLEAKSDVKOEPIISNYYAITSHTSLSALAH 86
 DB 60 PGGDLSVAPSVGLTANNEAWLMQIKEARADSEPALASYSTLSHSSLSRSLSP 119
 QY 87 ILTVKLSNINLPSNTLEFISVLESEPEIESTKODLIAVERDPACISYVHCFGEFG 146
 DB 120 HLGKLCSTLSTLTDLFNLISDSSLIDAVVADLRAARVRDPACVSFHSCLNLYKG 179
 QY 147 FLACQAHRIATLTKONKRIYALLIONRSESPAVDHPKAGIKGILDHATGVVIGET 206
 DB 180 FLACQSHRVAHKLNQDRPLALHRSIDVAVDHPKAGIKGILDHATGVVIGET 239
 QY 207 AVGDNYSILHGYTLGCTGKSGDRHPKIGDGVILGAGSCILGNTTIGKAGKSGSVYV 266
 DB 240 AITGDCSILHHTVLTGCTGKAGDRHPKVGDLVILGAGATILGNVILGKAGKSGSVL 299
 QY 267 KDVPARTAVGNPARKLGKGNPKRHKIPCLMDQTSYTEMSDYVI 314
 DB 300 IDVPRTTAVGNPARKLGKGNPKRHKIPCLMDQTSYTEMSDYVI 347

RESULT 6
 O9MAZ3 PRELIMINARY; PRT; 289 AA.
 AC O9MAZ3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN ASAT5.
 OS Allium tuberosum.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
 OX NCBI_TaxID=4683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Umano Y., Saito K.;
 RT "Allium tuberosum mRNA for serine acetyltransferase."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040502; BAA93050.1; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 289 AA; 30671 MW; 6DC2D784D25CF383 CRC64;

Query Match 53.1%; Score 872; DB 10; Length 289;
 Best Local Similarity 61.3%; Pred. No. 5.7e-63;
 Matches 166; Conservative 43; Mismatches 62; Indels 0; Gaps 0;

QY 44 DDDVYTKMLEAKSDVKOEPIISNYYAITSHTSLSALAHILSYKLSNINLPSNLF 103
 DB 19 DESWVWQIIAEARRADESEPALASYSTLSHPSLANSFHLANKLCSTLSTSLY 78
 QY 104 ELFTSVLESEPEIESTKODLIAVERDPACISYVHCFGEFGFLACQAHRIATLTKON 163
 DB 79 DFLNMLSTFTTILSKATVADLIAARHDPACIGFHSCLNLFKGFALVOTQRIAHVMSQS 138

QY 164 KTVALLIONRSESPAVDHPKAGIKGILDHATGVVIGETAVGDNYSILHGYTLG 223
 DB 139 RRLALALSRVADVSLVDHPKAGIKGILDHATGVVIGETAVIGNVSLHHTVLTG 198
 QY 224 TGKSGDRHPKIGDGVILGAGSCILGNTTIGKAGKSGSVVAVDVPARTAVGNPARI 283
 DB 199 TGKAGDRHPKIGDGVILGAGATILGNIRIGAGKAGKSGSVVILIDVPPRTTAVGNPARI 258
 QY 284 GKENPKRHKIPCLMDQTSYTEMSDYVI 314
 DB 259 GGEKPSMHEVPGESMDHTSFISMSDYII 289

RESULT 7
 O39533 PRELIMINARY; PRT; 294 AA.
 AC O39533;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN SAT.
 OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OX Cucurbitales; Cucurbitaceae; Citrullus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saito K., Inoue K., Fukushima R., Noji M.;
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-KINRO; TISSUE=GREEN LEAVES;
 RX MEDLINE=95332343; PubMed=7608200;
 RA Saito K., Yokoyama H., Noji M., Murakoshi I.;
 RT "Molecular cloning and characterization of a plant serine
 acetyltransferase playing a regulatory role in cysteine biosynthesis
 from watermelon."
 RT J. Biol. Chem. 270:16321-16326 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KINRO;
 RA Noji M., Inoue K., Saito K.;
 RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D85624; BAA12843.1; -
 DR EMBL: D49535; BAA08479.1; -
 DR EMBL: AB006530; BAA21827.1; -
 DR Mendel; 7748; Citla:1221; 7748.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 294 AA; 31537 MW; D9BA9667F638F86D CRC64;

Query Match 53.0%; Score 869; DB 10; Length 294;
 Best Local Similarity 58.6%; Pred. No. 1e-62;
 Matches 163; Conservative 49; Mismatches 66; Indels 0; Gaps 0;

QY 37 IHHTQIEDDDVWIKLEAKSDVKOEPIISNYYAITSHTSLSALAHILSYKLSNIN 96
 DB 17 VESTTNNDFTWLGQIKAEARRADESEPALASYSTLSHSSLSRSLSPHLGNKLCST 76
 QY 97 LPSNTLEFISVLESEPEIESTKODLIAVERDPACISYVHCFGEFGFLACQAHRIA 156
 DB 77 LSTLTLDLFNLFSTDYCLRSAYVADLQAAERDPACVSFHSCLNLYKGFLACQAHRA 136
 QY 157 HTLMKONKRIYALLIONRSESPAVDHPKAGIKGILDHATGVVIGETAVGDNYSIL 216
 DB 137 HKLMNSRRPLALQSRADVAVDHPKAGIKGILDHATGVVIGETAVIGNVSL 196

QY 217 HCVTIGGKSGDRHPIKIGDVLIGAGSCILNITIGEGAKIGSGSVYKVPARTAV 276
 DB 197 HAVTIGGKSGDRHPIKIGDVLIGAGATILNITIGEGAKIGAGSVYLDVPPRTAV 256
 QY 277 GNPARIKIGKPKRHKICITMDOTSTYLETSDYI 314
 DB 257 GNPARIKIGKPKRHKICITMDOTSTYLETSDYI 294

RESULT 8
 Q9SDP2 PRELIMINARY; PRT: 289 AA.
 AC Q9SDP2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE SERINE ACETYLTRANSFERASE.
 OS Allium cepa (Onion).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
 OX NCBI_TaxID=4679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. PUKEOHE LONG KEEPER; TISSUE=ROOT;
 RA Pither-Joyce M.D., McCallum J.A.;
 RT "Isolation of a serine acetyltransferase cDNA clone from Allium
 cepa."
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF212156; AAF19000.1;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase.
 SQ SEQUENCE 289 AA; 30574 MW; 9EA376C54DA0AF13 CRC64;

Query Match 52.5%; Score 861; DB 10; Length 289;
 Best Local Similarity 59.8%; Pred. No. 4.4e-62;
 Matches 162; Conservative 46; Mismatches 63; Indels 0; Gaps 0;
 QY 44 DDDVWIKMEAEKADYKOEPLISNYIYASTHSRLESALHILSKNLNLPSTLFI 103
 DB 19 DESWVWQIKRAKRDSEPALASTYITISHPSLARSLFHLANKLCSSTLSTSLY 78
 QY 104 ELFTSVLESESEITESTKODLIAVKEKDPACISYVHCFFKGFACQAHRIATLMKON 163
 DB 79 DLFNTLSTPEPYLSASVADLIAARHRDPACVGFSCCLNFKGFLAVQIRLAHVLSOS 138
 QY 164 KTIYALLIQRVSESPAVDHPGAKIGKGLLDHATGVYIGETAVGVNVSILHGVTLGG 223
 DB 139 RRPALALHSRVDVLSVDHPARIGKGLLDHAGVYIGETAVGVNVSILHGVTLGG 198
 QY 224 TCGQSDRHKIKIDGVYLIAGSCILNITIGEGAKIGSGSVYKVPARTAVGNPARI 283
 DB 199 TGAAGDHRHKIKIDGVYLIAGATILNIRIGAGAKVAGSVYLDVPPRTAVGNPARI 258
 QY 284 GKENRKHDKIKPCLNMDOTSTYLETSDYI 314
 DB 259 GKENRKHDKIKPCLNMDOTSTYLETSDYI 289

RESULT 9
 Q42538 PRELIMINARY; PRT: 312 AA.
 AC Q42538;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
 DE (SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52).
 SAT-52.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 CC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=97201050; PubMed=9048879;
 RA Howarth J.R., Roberts M.A., Wray J.L.;
 RT "Cysteine biosynthesis in higher plants: a new member of the
 Arabidopsis thaliana serine acetyltransferase small gene-family
 obtained by functional complementation of an Escherichia coli cysteine
 auxotroph."
 RT Biochim. Biophys. Acta 1350:123-127(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98403864; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones."
 RL DNA Res. 5:203-216(1998).
 DR EMBL: AB013392; BAB09894.1;
 DR EMBL: U30298; AAC49655.1;
 DR Mendel: 6699; Arabid.1221:6699.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 312 AA; 32770 MW; 15835510FF31A08 CRC64;

Query Match 51.8%; Score 849.5; DB 10; Length 312;
 Best Local Similarity 59.7%; Pred. No. 4.2e-61;
 Matches 160; Conservative 45; Mismatches 62; Indels 1; Gaps 1;
 QY 48 VWIKLEAKADYKOEPLISNYIYASTHSRLESALHILSKNLNLPSTLFI 107
 DB 45 LWTOKAEARDAEALASLYITISHSLERSISFLGNKLLSSTLSTLYDPL 104
 QY 108 SVLESESEITESTKODLIAVKEKDPACISYVHCFFKGFACQAHRIATLMKONRITV 167
 DB 105 NTFSSDPSLRNATYADLRARVADPACISVSCCLNFKGFLAVQIRLAHVLSOS 164
 QY 168 ALLIQRVSESPAVDHPGAKIGKGLLDHATGVYIGETAVGVNVSILHGVTLGG 227
 DB 165 ALALHSRISVFAVDHPGAKIGKGLLDHATGVYIGETAVGVNVSILHGVTLGG 224
 QY 228 SGRHPIKIGDVLIGAGSCILNITIGEGAKIGSGSVYKVPARTAVGNPARI 287
 DB 225 CGDRHPIKIGDVLIGAGATILNITIGEGAKIGAGSVYLDVPPRTAVGNPARI 284
 QY 288 NPKRKHDKIKPCLNMDOTSTYLETSDYI 314
 DB 285 KPTIHDECPGSMHTSTSEMSDYII 312

RESULT 10
 Q92PJ4 PRELIMINARY; PRT: 323 AA.
 AC Q92PJ4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).
 SAT-106.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OX NCBI_TaxID=3702;
 RN [1]

[illegible][illegible]

QY 200 GVYIGETAVVGDNVSILHGVTLGGTGKSGDRHPRIGEDGVILGAGSCLGNITIGGGAMV
 |||||||: : |||||||: : |||||||: : ||| ||||: ||| :
 Db 186 GVYIGETAVVGNVSILHGVTLGGTGKSGDRHPRIGEGALLGACVYTLGNISIGAGAMV

QY 200 GVYIGETAVVGDNVSILHGVTLGGTGKSGDRHPRIGEDGVILGAGSCLGNITIGGGAMV
 |||||||: : |||||||: : |||||||: : ||| ||||: ||| :
 Db 186 GVYIGETAVVGNVSILHGVTLGGTGKSGDRHPRIGEGALLGACVYTLGNISIGAGAMV

QY 260 GCGSVVKKVDPARTVAGNPARLIGKENPKRHKDKTPECLTM 300
 DB 246 AAGSLVKDVPSSHVYVAGNPAKLIRVME-----EQDPSILAM 281

RESULT 13

Q9JR86 PRELIMINARY; PRT; 272 AA.

AC Q9JR86;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE PUTATIVE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).
 GN CYSE OR NM00742 OR NM00560.
 OS Neisseria meningitidis (serogroup A), and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NX NCBI_TaxID=65699, 491;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=2491 / SEROGROUP A / SEROTYPE 4A;
 RC MEDLINE=2022556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
 Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
 Rajadurai M.A., Rutherford K.M., Simmonds M., Skelton J.,
 Whitehead S., Spratt B.G., Barrall B.G.;
 RT Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491."
 RL Nature 404:502-506(2000).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;
 RC MEDLINE=2017575; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Clifton E., Clark E.B.,
 Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58."
 RL Science 287:1809-1815(2000).
 DR EMBL: AL162754; CAB84026.1; -;
 DR EMBL: AE002412; AAF40988.1; -;
 DR TIGR: NMB0560; -;
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexaped; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KM Transferase: Acyltransferase.
 SO SEQUENCE 272 AA; 29399 MW; 4CB74D8A916386EB CRC64;

Query Match 39.6%; Score 649.5; DB 2; Length 272;
 Best Local Similarity 50.7%; Pred. No. 5,9e-45;
 Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

QY 47 DWIKMLEAKSDVKOEPLISNYVASTSHRSLESALAHILSVKLSINLPSTLFELE 106
 DB 12 LWHHTRETAAVASEPMASFLHQTVALRHESGLVLAHLSKIGSPIMDVRALEFY 71
 QY 107 ISVLESPEIISTKODLTAVERDPACISYVHCFEGFLACQAHRIAHILMKQNKRI 166
 DB 72 QQALGSDTOIGKVEADLATERDPACDEYSLPLTYFGFAIDAHRIHNLHYLDGRKT 131
 QY 167 VALLIONRSEFAVDIHGAKIGKILLDHAATGVVIGETAVAGNVSLHGLTGTGK 226
 DB 132 LAVFLGNRSEVAGVDIHRAARFGYGLMDHATGTAVAGTAVLGNISILHVTLTGSGSK 191
 QY 227 QSGDRPRKIGDGVLIAGSCILGNTTIGGAKIGSGSVVKKVDPARTVAGNPARLIGK 286

DB 192 ECGDRHPRKIGGVYMGANASTILGNIRIGSNNAKIGAGSVVSDVPSTIVGVPAKPAVA-- 249
 QY 287 ENPKRHKDKTPECLTMDOSTYLEMSDYVI 314
 DB 250 -----RSKTPSADMONTQTFE-IDFMT 272

RESULT 14

Q9KNT2 PRELIMINARY; PRT; 273 AA.

AC Q9KNT2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE SERINE ACETYLTRANSFERASE.
 GN VC2649.
 OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NX NCBI_TaxID=666;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N1961 / SEROTYPE O1;
 RC MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dracot I., Sellers P.,
 McDonald L., Uitterback T., Fleischmann R.D., Niernan W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL: AE004331; AAP95790.1; -;
 DR TIGR: VC2649; -;
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexaped; 4.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KM Transferase.
 SO SEQUENCE 273 AA; 29278 MW; 5CBEL6376B45B76F CRC64;

Query Match 39.5%; Score 647.5; DB 2; Length 273;
 Best Local Similarity 50.0%; Pred. No. 8,7e-45;
 Matches 132; Conservative 50; Mismatches 71; Indels 11; Gaps 3;

QY 39 HTQIEDDDDWIKMLEAKSDVKOEPLISNYVASTSHRSLESALAHILSVKLSINLP 98
 DB 6 HTK-----WQTVAAEREOAEQEPMLASFYHATIIKHDSLKAAISYILANRLNTASMP 59
 QY 99 SNTLFELEISVLESPEIISTKODLTAVERDPACISYVHCFEGFLACQAHRIAHIL 158
 DB 60 AMAYAEVTEEPAPADPSISEAACDICTVNRDPVANSYMPLLYLGLYHALQOYRAANW 119
 QY 159 LMKONRKIVALLIONRSEFAVDIHGAKIGKILLDHAATGVVIGETAVAGNVSLHGL 218
 DB 120 LMRGRKALAVYFQNGISVACQVDIHRAARIGRIMDHATGTAVAGTAVLGNISILH 179
 QY 219 VTLGTGKQSGDRHPRKIGDGVLIAGSCILGNTTIGGAKIGSGSVVKKVDPARTVAGN 278
 DB 180 VTLGTGKECGDRHPRKIGEGVIGAGAKIILGNTINVEGAKIGSGSVVLAQVPPHTVAGV 239
 QY 279 PARLIGKENPKRHKDKTPECLTMDQ 302
 DB 240 PARTVGRPOS---DK-PSLMDQ 258

RESULT 15

Q9SLZ8 PRELIMINARY; PRT; 402 AA.

ID Q9SLZ8;
 AC Q9SLZ8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
 DE SERINE ACETYLTRANSFERASE.
 GN CMTAT.
 OS Cyanidioschyzon merolae.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
 OX NCBI_TaxID=45157;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98288115; PubMed=9622597;
 RA Toda K., Takano H., Miyagishi S., Kuroiwa H., Kuroiwa T.;
 RT "Characterization of a chloroplast isoform of serine acetyltransferase
 from the thermo-acidophilic red alga Cyanidioschyzon merolae.";
 RL Biochim. Biophys. Acta 1403:72-84(1998).
 DR EMBL: AB006428; BAA88412.1; -.
 KW Transferase.
 SQ SEQUENCE 402 AA; 43739 MW; D97E69E8FF79F452 CRC64;

Query Match 38.4%; Score 629.5; DB 10; Length 402;
 Best Local Similarity 47.1%; Pred. No. 4.3e-43;
 Matches 130; Conservative 51; Mismatches 92; Indels 3; Gaps 2;

QY 27 FRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDVKQEPILSNYYASITSHRSLESALAH 86
 Db 97 FGPIVISVDNW-RTLIYSSDPWVELVRREAIGANEPOPLASSLVAFLNHRCTEDTLAF 155
 QY 87 ILSVKLSNMLPNSNTLELFISVLESPELIEESTKODLIAVKERDPACISYVHCFLGFG 146
 Db 156 HLANELASPEFOATQYVKLFRDALYQDKSYREAIRADLAVRRDPAMKRCVAVLMYSKG 215
 QY 147 FLACQAHRIAHITLWKONRKIVALLIONRVSESPAVDIHPGAKIGKGLLDHATGVIGET 206
 Db 216 YALQATRLHLHLRQDRKVALFLQSEISKCPAVDIHPAKIGSGVWIDHATGIVIGET 275
 QY 207 AVYGDNVSLHGYTLGGTGKQSGDRHPRKIGDGVLIAGSCILGNITIGGAKIGSGSVVY 266
 Db 276 AVYGNDVSMHLNVTLLGGTGKQSGDRHPRKIGDGVLIAGSCILGNITIGGAKIGSGSVVY 335
 QY 267 KDVPAARTAVGNPARLIGKENPRKHDKIPCLTMDQ 302
 Db 336 KDVPPYITVSGVPAREVYGLKLSYPR--GVYPAFEMDQ 369

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